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Sequence Listing was accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: [year=2009; month=8; day=14; hr=8; min=9; sec=16; ms=907; ]
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Validated By CRFValidator v 1.0.3
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Application No: 10539723   Version No: 2.0

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<110>   Bayer CropScience GmbH
         Hoehne, Michaela
         Frohberg, Claus
         Landschuetze, Volker

<120>   Plant cells and plants which synthesize a starch with an
         increased final viscosity

<130>   65084.000013

<140>   10539723
<141>   2005-06-20

<150>   EP 02028530.0
<151>   2002-12-19

<150>   PCT/EP03/14840
<151>   2003-12-19

<150>   EP 03090275.3
<151>   2003-08-29

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<170>   PatentIn version 3.5

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<212>   DNA

<213>   Solanum tuberosum

<220>

<221>   CDS

<222>   (207)..(3899)

<300>

<301>   Abel,G.J., Springer,F., Willmitzer,L. and Kossmann,J.

<302>   Cloning and functional analysis of a cDNA encoding a novel 139 kDa

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gatgttctat ttgattctgt ggtgaacaag agttttacaa agaacattcc ttttttcttt   180

tttcttggtt cttgtgtggg tcagcc atg gat gtt cca ttt cca ctg cat aga   233
                              Met Asp Val Pro Phe Pro Leu His Arg
                               1   5

cca ttg agt tgc aca agt gtc tcc aat gca ata acc cac ctc aag atc   281
Pro Leu Ser Cys Thr Ser Val Ser Asn Ala Ile Thr His Leu Lys Ile
10   15   20   25

aaa cct ttt ctt ggg ttt gtc tct cat gga acc aca agt cta tca gta   329
Lys Pro Phe Leu Gly Phe Val Ser His Gly Thr Thr Ser Leu Ser Val
                30   35   40

caa tct tct tca tgg agg aag gat gga atg gtt act ggg gtt tca ttt   377
Gln Ser Ser Ser Trp Arg Lys Asp Gly Met Val Thr Gly Val Ser Phe
            45   50   55

cca ttt tgt gca aat ctc tcg gga aga aga cgg aga aaa gtt tca act   425
Pro Phe Cys Ala Asn Leu Ser Gly Arg Arg Arg Arg Lys Val Ser Thr
        60   65   70

act agg agt caa gga tct tca cct aag ggg ttt gtg cca agg aag ccc   473
Thr Arg Ser Gln Gly Ser Ser Pro Lys Gly Phe Val Pro Arg Lys Pro

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Ser Gly Met Ser Thr Gln Arg Lys Val Gln Lys Ser Asn Gly Asp Lys
 90                  95                 100                 105

gaa agt caa agt act tca aca tct aaa gaa tct gaa att tcc aac cag        569
Glu Ser Gln Ser Thr Ser Thr Ser Lys Glu Ser Glu Ile Ser Asn Gln
                    110                 115                 120

aag acg gtt gaa gca aga gtt gaa act agt gac gat gac act aaa gta        617
Lys Thr Val Glu Ala Arg Val Glu Thr Ser Asp Asp Asp Thr Lys Val
            125                 130                 135

gtg gtg agg gac cac aag ttt ctg gag gat gag gat gaa atc aat ggt        665
Val Val Arg Asp His Lys Phe Leu Glu Asp Glu Asp Glu Ile Asn Gly
        140                 145                 150

tct act aaa tca ata agt atg tca cct gtt cgt gta tca tct caa ttt        713
Ser Thr Lys Ser Ile Ser Met Ser Pro Val Arg Val Ser Ser Gln Phe
        155                 160                 165

gtt gaa agt gaa gaa act ggt ggt gat gac aag gat gct gta aag tta        761
Val Glu Ser Glu Glu Thr Gly Gly Asp Asp Lys Asp Ala Val Lys Leu
170                 175                 180                 185

aac aaa tca aag aga tcg gaa gag agt gat ttt cta att gat tct gta        809
Asn Lys Ser Lys Arg Ser Glu Glu Ser Asp Phe Leu Ile Asp Ser Val
                    190                 195                 200

ata aga gaa caa agt gga tct cag ggg gaa act aat gcc agt agc aag        857
Ile Arg Glu Gln Ser Gly Ser Gln Gly Glu Thr Asn Ala Ser Ser Lys
                    205                 210                 215

gga agc cat gct gtg ggt aca aaa ctt tat gag ata ttg cag gtg gat        905
Gly Ser His Ala Val Gly Thr Lys Leu Tyr Glu Ile Leu Gln Val Asp
        220                 225                 230

gtt gag cca caa caa ttg aaa gaa aat aat gct ggg aat gtt gaa tac        953
Val Glu Pro Gln Gln Leu Lys Glu Asn Asn Ala Gly Asn Val Glu Tyr
        235                 240                 245

aaa gga cct gta gca agt aag cta ttg gaa att act aag gct agt gat       1001
Lys Gly Pro Val Ala Ser Lys Leu Leu Glu Ile Thr Lys Ala Ser Asp
250                 255                 260                 265

gtg gaa cac act gaa agc aat gag att gat gac tta gac act aat agt       1049
Val Glu His Thr Glu Ser Asn Glu Ile Asp Asp Leu Asp Thr Asn Ser
                    270                 275                 280

ttc ttt aaa tca gat tta att gaa gag gat gag cca tta gct gca gga       1097
Phe Phe Lys Ser Asp Leu Ile Glu Glu Asp Glu Pro Leu Ala Ala Gly
                    285                 290                 295

aca gtg gag act gga gat tct tct cta aac tta aga ttg gag atg gaa       1145
Thr Val Glu Thr Gly Asp Ser Ser Leu Asn Leu Arg Leu Glu Met Glu
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gca aat cta cgt agg cag gct ata gaa agg ctt gcc gag gaa aat tta   1193
Ala Asn Leu Arg Arg Gln Ala Ile Glu Arg Leu Ala Glu Glu Asn Leu
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ttg caa ggg atc aga tta ttt tgt ttt cca gag gtt gta aaa cct gat   1241
Leu Gln Gly Ile Arg Leu Phe Cys Phe Pro Glu Val Val Lys Pro Asp
330   335   340   345

gaa gat gtc gag ata ttt ctt aac aga ggt ctt tcc act ttg aag aat   1289
Glu Asp Val Glu Ile Phe Leu Asn Arg Gly Leu Ser Thr Leu Lys Asn
                350   355   360

gag tct gat gtc ttg att atg gga gct ttt aat gag tgg cgc tat agg   1337
Glu Ser Asp Val Leu Ile Met Gly Ala Phe Asn Glu Trp Arg Tyr Arg
                365   370   375

tct ttt act aca agg cta act gag act cat ctc aat gga gat tgg tgg   1385
Ser Phe Thr Thr Arg Leu Thr Glu Thr His Leu Asn Gly Asp Trp Trp
            380   385   390

tct tgc aag atc cat gtt ccc aag gaa gca tac agg gct gat ttt gtg   1433
Ser Cys Lys Ile His Val Pro Lys Glu Ala Tyr Arg Ala Asp Phe Val
        395   400   405

ttt ttt aat gga caa gat gtc tat gac aac aat gat gga aat gac ttc   1481
Phe Phe Asn Gly Gln Asp Val Tyr Asp Asn Asn Asp Gly Asn Asp Phe
410   415   420   425

agt ata act gtg aaa ggt ggt atg caa atc att gac ttt gaa aat ttc   1529
Ser Ile Thr Val Lys Gly Gly Met Gln Ile Ile Asp Phe Glu Asn Phe
                430   435   440

ttg ctt gag gag aaa tgg aga gaa cag gag aaa ctt gct aaa gaa caa   1577
Leu Leu Glu Glu Lys Trp Arg Glu Gln Glu Lys Leu Ala Lys Glu Gln
                445   450   455

gct gaa aga gaa aga cta gcg gaa gaa caa aga cga ata gaa gca gag   1625
Ala Glu Arg Glu Arg Leu Ala Glu Glu Gln Arg Arg Ile Glu Ala Glu
            460   465   470

aaa gct gaa att gaa gct gac aga gca caa gca aag gaa gag gct gca   1673
Lys Ala Glu Ile Glu Ala Asp Arg Ala Gln Ala Lys Glu Glu Ala Ala
    475   480   485

aag aaa aag aaa gta ttg cga gaa ttg atg gta aaa gcc acg aag act   1721
Lys Lys Lys Lys Val Leu Arg Glu Leu Met Val Lys Ala Thr Lys Thr
490   495   500   505

cgt gat atc acg tgg tac ata gag cca agt gaa ttt aaa tgc gag gac   1769
Arg Asp Ile Thr Trp Tyr Ile Glu Pro Ser Glu Phe Lys Cys Glu Asp
                510   515   520

aag gtc agg tta tac tat aac aaa agt tca ggt cct ctc tcc cat gct   1817
Lys Val Arg Leu Tyr Tyr Asn Lys Ser Ser Gly Pro Leu Ser His Ala
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aag gac ttg tgg atc cac gga gga tat aat aat tgg aag gat ggt ttg          1865
Lys Asp Leu Trp Ile His Gly Gly Tyr Asn Asn Trp Lys Asp Gly Leu
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tct att gtc aaa aag ctt gtt aaa tct gag aga ata gat ggt gat tgg          1913
Ser Ile Val Lys Lys Leu Val Lys Ser Glu Arg Ile Asp Gly Asp Trp
    555                 560                 565

tgg tat aca gag gtt gtt att cct gat cag gca ctt ttc ttg gat tgg          1961
Trp Tyr Thr Glu Val Val Ile Pro Asp Gln Ala Leu Phe Leu Asp Trp
570                 575                 580                 585

gtt ttt gct gat ggt cca ccc aag cat gcc att gct tat gat aac aat          2009
Val Phe Ala Asp Gly Pro Pro Lys His Ala Ile Ala Tyr Asp Asn Asn
                590                 595                 600

cac cgc caa gac ttc cat gcc att gtc ccc aac cac att ccg gag gaa          2057
His Arg Gln Asp Phe His Ala Ile Val Pro Asn His Ile Pro Glu Glu
                605                 610                 615

tta tat tgg gtt gag gaa gaa cat cag atc ttt aag aca ctt cag gag          2105
Leu Tyr Trp Val Glu Glu Glu His Gln Ile Phe Lys Thr Leu Gln Glu
        620                 625                 630

gag aga agg ctt aga gaa gcg gct atg cgt gct aag gtt gaa aaa aca          2153
Glu Arg Arg Leu Arg Glu Ala Ala Met Arg Ala Lys Val Glu Lys Thr
    635                 640                 645

gca ctt ctg aaa act gaa aca aag gaa aga act atg aaa tca ttt tta          2201
Ala Leu Leu Lys Thr Glu Thr Lys Glu Arg Thr Met Lys Ser Phe Leu
650                 655                 660                 665

ctg tct cag aag cat gta gta tat act gag cct ctt gat atc caa gct          2249
Leu Ser Gln Lys His Val Val Tyr Thr Glu Pro Leu Asp Ile Gln Ala
                670                 675                 680

gga agc agc gtc aca gtt tac tat aat ccc gcc aat aca gta ctt aat          2297
Gly Ser Ser Val Thr Val Tyr Tyr Asn Pro Ala Asn Thr Val Leu Asn
                685                 690                 695

ggt aaa cct gaa att tgg ttc aga tgt tca ttt aat cgc tgg act cac          2345
Gly Lys Pro Glu Ile Trp Phe Arg Cys Ser Phe Asn Arg Trp Thr His
        700                 705                 710

cgc ctg ggt cca ttg cca cct cag aaa atg tcg cct gct gaa aat ggc          2393
Arg Leu Gly Pro Leu Pro Pro Gln Lys Met Ser Pro Ala Glu Asn Gly
        715                 720                 725

acc cat gtc aga gca act gtg aag gtt cca ttg gat gca tat atg atg          2441
Thr His Val Arg Ala Thr Val Lys Val Pro Leu Asp Ala Tyr Met Met
730                 735                 740                 745

gat ttt gta ttt tcc gag aga gaa gat ggt ggg att ttt gac aat aag          2489
Asp Phe Val Phe Ser Glu Arg Glu Asp Gly Gly Ile Phe Asp Asn Lys
                750                 755                 760

agc gga atg gac tat cac ata cct gtg ttt gga gga gtc gct aaa gaa          2537
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Ser Gly Met Asp Tyr His Ile Pro Val Phe Gly Gly Val Ala Lys Glu
        765   770   775

cct cca atg cat att gtc cat att gct gtc gaa atg gca cca att gca   2585
Pro Pro Met His Ile Val His Ile Ala Val Glu Met Ala Pro Ile Ala
        780   785   790

aag gtg gga ggc ctt ggt gat gtt gtt act agt ctt tcc cgt gct gtt   2633
Lys Val Gly Gly Leu Gly Asp Val Val Thr Ser Leu Ser Arg Ala Val
        795   800   805

caa gat tta aac cat aat gtg gat att atc tta cct aag tat gac tgt   2681
Gln Asp Leu Asn His Asn Val Asp Ile Ile Leu Pro Lys Tyr Asp Cys
810   815   820   825

ttg aag atg aat aat gtg aag gac ttt cgg ttt cac aaa aac tac ttt   2729
Leu Lys Met Asn Asn Val Lys Asp Phe Arg Phe His Lys Asn Tyr Phe
              830   835   840

tgg ggt ggg act gaa ata aaa gta tgg ttt gga aag gtg gaa ggt ctc   2777
Trp Gly Gly Thr Glu Ile Lys Val Trp Phe Gly Lys Val Glu Gly Leu
             845   850   855

tcg gtc tat ttt ttg gag cct caa aac ggg tta ttt tcg aaa ggg tgc   2825
Ser Val Tyr Phe Leu Glu Pro Gln Asn Gly Leu Phe Ser Lys Gly Cys
          860   865   870

gtc tat ggt tgt agc aat gat ggt gaa cga ttt ggt ttc ttc tgt cac   2873
Val Tyr Gly Cys Ser Asn Asp Gly Glu Arg Phe Gly Phe Phe Cys His
        875   880   885

gcg gct ttg gag ttt ctt ctg caa ggt gga ttt agt ccg gat atc att   2921
Ala Ala Leu Glu Phe Leu Leu Gln Gly Gly Phe Ser Pro Asp Ile Ile
890   895   900   905

cat tgc cat gat tgg tct agt gct cct gtt gct tgg ctc ttt aag gaa   2969
His Cys His Asp Trp Ser Ser Ala Pro Val Ala Trp Leu Phe Lys Glu
              910   915   920

caa tat aca cac tat ggt cta agc aaa tct cgt ata gtc ttc acg ata   3017
Gln Tyr Thr His Tyr Gly Leu Ser Lys Ser Arg Ile Val Phe Thr Ile
          925   930   935

cat aat ctt gaa ttt ggg gca gat ctc att ggg aga gca atg act aac   3065
His Asn Leu Glu Phe Gly Ala Asp Leu Ile Gly Arg Ala Met Thr Asn
        940   945   950

gca gac aaa gct aca aca gtt tca cca act tac tca cag gag gtg tct   3113
Ala Asp Lys Ala Thr Thr Val Ser Pro Thr Tyr Ser Gln Glu Val Ser
        955   960   965

gga aac cct gta att gcg cct cac ctt cac aag ttc cat ggt ata gtg   3161
Gly Asn Pro Val Ile Ala Pro His Leu His Lys Phe His Gly Ile Val
970   975   980   985

aat ggg att gac cca gat att tgg gat cct tta aac gat aag ttc   att   3209
Asn Gly Ile Asp Pro Asp Ile Trp Asp Pro Leu Asn Asp Lys Phe   Ile

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ccg att ccg tac  acc tca gaa aac gtt  gtt gaa ggc aaa aca  gca    3254
Pro Ile Pro Tyr  Thr Ser Glu Asn Val  Val Glu Gly Lys Thr  Ala
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gcc aag gaa gct  ttg cag cga aaa ctt  gga ctg aaa cag gct  gac    3299
Ala Lys Glu Ala  Leu Gln Arg Lys Leu  Gly Leu Lys Gln Ala  Asp
            1020              1025              1030

ctt cct ttg gta  gga att atc acc cgc  tta act cac cag aaa  gga    3344
Leu Pro Leu Val  Gly Ile Ile Thr Arg  Leu Thr His Gln Lys  Gly
            1035              1040              1045

atc cac ctc att  aaa cat gct att tgg  cgc acc ttg gaa cgg  aac    3389
Ile His Leu Ile  Lys His Ala Ile Trp  Arg Thr Leu Glu Arg  Asn
            1050              1055              1060

gga cag gta gtc  ttg ctt ggt tct gct  cct gat cct agg gta  caa    3434
Gly Gln Val Val  Leu Leu Gly Ser Ala  Pro Asp Pro Arg Val  Gln
            1065              1070              1075

aac gat ttt gtt  aat ttg gca aat caa  ttg cac tcc aaa tat  aat    3479
Asn Asp Phe Val  Asn Leu Ala Asn Gln  Leu His Ser Lys Tyr  Asn
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gac cgc gca cga  ctc tgt cta aca tat  gac gag cca ctt tct  cac    3524
Asp Arg Ala Arg  Leu Cys Leu Thr Tyr  Asp Glu Pro Leu Ser  His
            1095              1100              1105

ctg ata tat gct  ggt gct gat ttt att  cta gtt cct tca ata  ttt    3569
Leu Ile Tyr Ala  Gly Ala Asp Phe Ile  Leu Val Pro Ser Ile  Phe
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gag cca tgt gga  cta aca caa ctt acc  gct atg aga tat ggt  tca    3614
Glu Pro Cys Gly  Leu Thr Gln Leu Thr  Ala Met Arg Tyr Gly  Ser
            1125              1130              1135

att cca gtc gtg  cgt aaa act gga gga  ctt tat gat act gta  ttt    3659
Ile Pro Val Val  Arg Lys Thr Gly Gly  Leu Tyr Asp Thr Val  Phe
            1140              1145              1150

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Asp Val Asp His  Asp Lys Glu Arg Ala  Gln Gln Cys Gly Leu  Glu
            1155              1160              1165

cca aat gga ttc  agc ttt gat gga gca  gat gct ggc gga gtt  gat    3749
Pro Asn Gly Phe  Se
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